AMENDMENTS TO THE CLAIMS

1. (Original) A method for the detection of the presence of or the risk of cancer in a patient comprising the steps of: (i) isolating a sample of the patient's genome; and (ii) detecting the presence or expression of the gene comprised within the sequence identified herein as SEQ ID No. 1, wherein the presence or expression of the gene indicates the presence of or the risk of cancer.

2. (Original) A method according to claim 1, wherein the gene is that identified as SEQ ID No. 2.

3. (Original) A method according to claim 1 or claim 2, wherein the genome sample is obtained from breast tissue, the uterus or testis.

4. (Currently Amended) A method according to ~~any preceding claim~~ claim 1, wherein the cancer is breast cancer.

5. (Currently Amended) A method according to ~~any preceding claim~~ claim 1, wherein detection is carried out by amplifying the gene using the polymerase enzyme.

6. (Original) An isolated polynucleotide comprising the nucleotide sequence identified herein as SEQ ID No. 1, or its complement, or a polynucleotide of at least 15 consecutive nucleotides that hybridises to the sequence (or its complement) under stringent hybridising conditions.

7. (Original) An isolated polynucleotide according to claim 6, wherein the sequence is that identified herein as SEQ ID No. 2.

8. (Currently Amended) ~~Use of a polynucleotide according to claim 6 or claim 7, in an *in vitro* diagnostic assay to test for the risk of cancer in a patient.~~ A method according to claim 1 wherein the detecting comprises performing an *in vitro* hybridization assay with the sample of the patient's genome and an isolated polynucleotide comprising at least 15 consecutive nucleotides of SEQ ID No. 1, or its complement, as a hybridization probe to detect the presence of or the risk of cancer in the patient.

9. (Currently Amended) ~~Use~~ A method according to claim 8, wherein the cancer is breast cancer.

10. (Original) A peptide comprising the sequence identified herein as SEQ ID No. 3, or a fragment thereof of at least 10 consecutive amino acid residues.

11. (Original) An antibody having an affinity of at least 10^{-6}M for the peptide of claim 10.

12. (Original) Use of a second polynucleotide that hybridises with or inhibits the expression of an endogenous gene that comprises the polynucleotide of claim 6 or claim 7, in the manufacture of a medicament for the treatment of cancer, in particular breast cancer.

13. (Original) Use according to claim 12, wherein the gene comprises the polynucleotide of claim 7.

14. (New) A method according to claim 1 wherein the detecting comprises performing an *in vitro* hybridization assay with the sample of the patient's genome and an isolated polynucleotide comprising at least 15 consecutive nucleotides of SEQ ID No. 2, or its complement, as a hybridization probe to detect the presence of or the risk of cancer in the patient.

15. (New) A method according to claim 14, wherein the cancer is breast cancer.